

SEQUENCE LISTING

<110> NARIMATSU, Hisashi et al.

<120> NOVEL N-ACETYLGLUCOSAMINE TRANSFERASE, NUCLEIC ACID ENCODING THE SAME AND USE THEREOF IN DIAGNOSING CANCER AND/OR TUMOR

<130> 0760-0337PUS1

<140> US 10/507,421

<141> 2004-09-13

<150> PCT/JP03/03044

<151> 2003-03-14

<150> JP 2002-70996

<151> 2002-03-14

<160> 28

<170> PatentIn 3.2

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<213> Homo sapiens

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Gly Arg Gly Ala Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys
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Leu Thr Leu Lys Glu Ile His Phe Leu Lys Trp Leu Asp Ile Tyr Cys
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Pro His Val Pro Phe Ile Phe Lys Gly Asp Asp Asp Val Phe Val Asn
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Pro Thr Asn Leu Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn
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Asp Asn Lys Tyr Tyr Ile Pro Gly Ala Leu Tyr Gly Lys Ala Ser Tyr
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 Gly Arg Gly Ala Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys
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 Pro His Val Pro Phe Ile Phe Lys Gly Asp Asp Asp Val Phe Val Asn
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 Pro Thr Asn Leu Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn
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Arg Met Asn Lys Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His	
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Lys Leu Leu Pro Pro Glu Leu Leu Ala Met Trp Gly Leu Val His Ser	
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245 250 255	
Gly Met Cys Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu Gly	
260 265 270	
Phe Lys Thr Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn Lys	
275 280 285	
Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu Pro	
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 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val
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 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg
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 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala
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 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg
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 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp
 115 120 125
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 Ile Leu Gln Trp Gly Phe Leu Asp Thr Phe Phe Asn Leu Thr Leu Lys
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 Asp Val Leu Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr
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 Tyr Ile Pro Gly Ala Leu Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr Ala
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 225 230 235 240
 cat gcc tgc gac acc ctg gag ctc tac ccg atc gac gac gtc ttt ctg 768

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Gly	Met	Cys	Leu	Glu	Val	Leu	Gly	Val	Gln	Pro	Thr	Ala	His	Glu	Gly	
			260					265					270			
ttc	aag	act	ttc	ggc	atc	tcc	cgg	aac	cgc	aac	agc	cgc	atg	aac	aag	864
Phe	Lys	Thr	Phe	Gly	Ile	Ser	Arg	Asn	Arg	Asn	Ser	Arg	Met	Asn	Lys	
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gag	ccg	tgc	ttt	ttc	cgc	gcc	atg	ctc	gtg	gtg	cac	aag	ctg	ctg	ccc	912
Glu	Pro	Cys	Phe	Phe	Arg	Ala	Met	Leu	Val	Val	His	Lys	Leu	Leu	Pro	
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Pro	Glu	Leu	Leu	Ala	Met	Trp	Gly	Leu	Val	His	Ser	Asn	Leu	Thr	Cys	
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Gln	Phe	Leu	Gln	Glu	Pro	Pro	Pro	Pro	Thr	Leu	Glu	Pro	Gln	Lys	Ala	
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Gln	Lys	Pro	Asn	Gly	Gln	Leu	Val	Asn	Pro	Asn	Asn	Phe	Trp	Lys	Asn	
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ccg	aaa	gat	gtg	gct	gcg	ccc	acg	ccc	atg	gcc	tct	cag	ggg	ccc	cag	240
Pro	Lys	Asp	Val	Ala	Ala	Pro	Thr	Pro	Met	Ala	Ser	Gln	Gly	Pro	Gln	
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gcc	tgg	gac	gtg	acc	acc	act	aac	tgc	tca	gcc	aat	atc	aac	ttg	acc	288
Ala	Trp	Asp	Val	Thr	Thr	Thr	Asn	Cys	Ser	Ala	Asn	Ile	Asn	Leu	Thr	
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cac	cag	ccc	tgg	ttc	cag	gtc	ctg	gag	ccg	cag	ttc	cgc	cag	ttt	ctc	336
His	Gln	Pro	Trp	Phe	Gln	Val	Leu	Glu	Pro	Gln	Phe	Arg	Gln	Phe	Leu	
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Phe	Tyr	Arg	His	Cys	Arg	Tyr	Phe	Pro	Met	Leu	Leu	Asn	His	Pro	Glu	
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Lys	Cys	Arg	Gly	Asp	Val	Tyr	Leu	Leu	Val	Val	Val	Lys	Ser	Val	Ile	
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Thr	Gln	His	Asp	Arg	Arg	Glu	Ala	Ile	Arg	Gln	Thr	Trp	Gly	Arg	Glu	
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Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp Ile Leu Gln Trp Gly Phe	
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Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr Tyr Ile Pro Gly Ala Leu	
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Cys Arg Tyr	Phe Pro Met	Leu Leu Asn	His Pro Glu	Lys Cys Arg	Gly	
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Arg Arg Glu	Ala Ile Arg	Gln Thr Trp	Gly Arg Glu	Arg Gln Ser	Ala	
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Gly Gly Gly	Arg Gly Ala	Val Arg Thr	Leu Phe Leu	Leu Gly Thr	Ala	
	95	100	105			
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Ser Lys Gln	Glu Glu Arg	Thr His Tyr	Gln Gln Leu	Leu Ala Tyr	Glu	
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Asp Arg Leu	Tyr Gly Asp	Ile Leu Gln	Trp Gly Phe	Leu Asp Thr	Phe	
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ttc aac ctg	acc ctc aag	gag atc cac	ttc ctc aag	tgg ctg gac	atc	2103
Phe Asn Leu	Thr Leu Lys	Glu Ile His	Phe Leu Lys	Trp Leu Asp	Ile	
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tac tgc ccc	cac gtc ccc	ttc att ttc	aaa ggc gac	gat gac gtc	ttc	2151
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gtc aac ccc	acc aac ctg	cta gaa ttt	ctg gct gac	cgg cag cca	cag	2199
Val Asn Pro	Thr Asn Leu	Leu Glu Phe	Leu Ala Asp	Arg Gln Pro	Gln	
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 <211> 848
 <212> DNA
 <213> Homo sapiens

<400> 7	
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Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp Ile Leu Gln	
1 5 10 15	
tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag gag atc cac	96
Trp Gly Phe Leu Asp Thr Phe Phe Asn Leu Thr Leu Lys Glu Ile His	
20 25 30	
ttc ctc aag tgg ctg gac atc tac tgc ccc cac gtc ccc ttc att ttc	144
Phe Leu Lys Trp Leu Asp Ile Tyr Cys Pro His Val Pro Phe Ile Phe	
35 40 45	
aaa ggc gac gat gac gtc ttc gtc aac ccc acc aac ctg cta gaa ttt	192
Lys Gly Asp Asp Asp Val Phe Val Asn Pro Thr Asn Leu Leu Glu Phe	
50 55 60	
ctg gct gac cgg cag cca cag gaa aac ctg ttc gtg ggc gat gtc ctg	240
Leu Ala Asp Arg Gln Pro Gln Glu Asn Leu Phe Val Gly Asp Val Leu	
65 70 75 80	
cag cac gct cgg ccc att cgc agg aaa gac aac aaa tac tac atc ccg	288
Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr Tyr Ile Pro	
85 90 95	
ggg gcc ctg tac ggc aag gcc agc tat ccg ccg tat gca ggc ggc ggt	336
Gly Ala Leu Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr Ala Gly Gly Gly	
100 105 110	
ggc ttc ctc atg gcc ggc agc ctg gcc cgg cgc ctg cac cat gcc tgc	384
Gly Phe Leu Met Ala Gly Ser Leu Ala Arg Arg Leu His His Ala Cys	
115 120 125	
gac acc ctg gag ctc tac ccg atc gac gac gtc ttt ctg ggc atg tgc	432
Asp Thr Leu Glu Leu Tyr Pro Ile Asp Asp Val Phe Leu Gly Met Cys	
130 135 140	
ctg gag gtg ctg ggc gtg cag ccc acg gcc cac gag ggc ttc aag act	480
Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu Gly Phe Lys Thr	
145 150 155 160	
ttc ggc atc tcc cgg aac cgc aac agc cgc atg aac aag gag ccg tgc	528
Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn Lys Glu Pro Cys	
165 170 175	
ttt ttc cgc gcc atg ctc gtg gtg cac aag ctg ctg ccc cct gag ctg	576
Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu Pro Pro Glu Leu	
180 185 190	
ctc gcc atg tgg ggg ctg gtg cac agc aat ctc acc tgc tcc cgc aag	624
Leu Ala Met Trp Gly Leu Val His Ser Asn Leu Thr Cys Ser Arg Lys	
195 200 205	
ctc cag gtg ctc tgacccacgc cgggctacta ggacaggcca gggcacttgc	676
Leu Gln Val Leu	
210	
tcttgagccc ccatggtatt ggggctggag ccacagtgcc caggcctagc ctttgggtccc	736
caaggggagg tggaggggtt aggcctacgt gccactgggt gtgggtgggt gcaggtagcc	796
agaaagggac ctccctgtgt ggataattct aggaaactga ggcccaggaa cg	848

<210> 8
 <211> 987
 <212> DNA
 <213> Homo sapiens

<400> 8
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 1 5 10 15
 tca gcc aat atc aac ttg acc cac cag ccc tgg ttc cag gtc ctg gag 96
 Ser Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu
 20 25 30
 ccg cag ttc cgg cag ttt ctc ttc tac cgc cac tgc cgc tac ttc ccc 144
 Pro Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro
 35 40 45
 atg ctg ctg aac cac ccg gag aag tgc agg ggc gat gtc tac ctg ctg 192
 Met Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu
 50 55 60
 gtg gtt gtc aag tcg gtc atc acg cag cac gac cgc cgc gag gcc atc 240
 Val Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile
 65 70 75 80
 cgc cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc 288
 Arg Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly
 85 90 95
 gcc gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag 336
 Ala Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu
 100 105 110
 cgc acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc 384
 Arg Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly
 115 120 125
 gac atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc 432
 Asp Ile Leu Gln Trp Gly Phe Leu Asp Thr Phe Phe Asn Leu Thr Leu
 130 135 140
 aag gag atc cac ttc ctc aag tgg ctg gac atc tac tgc ccc cac gtc 480
 Lys Glu Ile His Phe Leu Lys Trp Leu Asp Ile Tyr Cys Pro His Val
 145 150 155 160
 ccc ttc att ttc aaa ggc gac gat gac gtc ttc gtc aac ccc acc aac 528
 Pro Phe Ile Phe Lys Gly Asp Asp Asp Val Phe Val Asn Pro Thr Asn
 165 170 175
 ctg cta gaa ttt ctg gct gac cgg cag cca cag gaa aac ctg ttc gtg 576
 Leu Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn Leu Phe Val
 180 185 190
 ggc gat gtc ctg cag cac gct cgg ccc att cgc agg aaa gac aac aaa 624
 Gly Asp Val Leu Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asn Lys
 195 200 205
 tac tac atc ccg ggg gcc ctg tac ggc aag gcc agc tat ccg ccg tat 672
 Tyr Tyr Ile Pro Gly Ala Leu Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr
 210 215 220
 gca ggc ggc ggt ggc ttc ctc atg gcc ggc agc ctg gcc cgg cgc ctg 720
 Ala Gly Gly Gly Gly Phe Leu Met Ala Gly Ser Leu Ala Arg Arg Leu
 225 230 235 240
 cac cat gcc tgc gac acc ctg gag ctc tac ccg atc gac gac gtc ttt 768
 His His Ala Cys Asp Thr Leu Glu Leu Tyr Pro Ile Asp Asp Val Phe
 245 250 255
 ctg ggc atg tgc ctg gag gtg ctg ggc gtg cag ccc acg gcc cac gag 816
 Leu Gly Met Cys Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu
 260 265 270

ggc ttc aag act ttc ggc atc tcc cgg aac cgc aac agc cgc atg aac	864
Gly Phe Lys Thr Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn	
275 280 285	
aag gag ccg tgc ttt ttc cgc gcc atg ctc gtg gtg cac aag ctg ctg	912
Lys Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu	
290 295 300	
ccc cct gag ctg ctc gcc atg tgg ggg ctg gtg cac agc aat ctc acc	960
Pro Pro Glu Leu Leu Ala Met Trp Gly Leu Val His Ser Asn Leu Thr	
305 310 315 320	
tgc tcc cgc aag ctc cag gtg ctc tga	987
Cys Ser Arg Lys Leu Gln Val Leu	
325	

<210> 9
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 9

Met Ser Leu Trp Lys Lys Thr Val Tyr Arg Ser Leu Cys Leu Ala Leu	
1 5 10 15	
Ala Leu Leu Val Ala Val Thr Val Phe Gln Arg Ser Leu Thr Pro Gly	
20 25 30	
Gln Phe Leu Gln Glu Pro Pro Pro Pro Thr Leu Glu Pro Gln Lys Ala	
35 40 45	
Gln Lys Pro Asn Gly Gln Leu Val Asn Pro Asn Asn Phe Trp Lys Asn	
50 55 60	
Pro Lys Asp Val Ala Ala Pro Thr Pro Met Ala Ser Gln Gly Pro Gln	
65 70 75 80	
Ala Trp Asp Val Thr Thr Thr Asn Cys Ser Ala Asn Ile Asn Leu Thr	
85 90 95	
His Gln Pro Trp Phe Gln Val Leu Glu Pro Gln Phe Arg Gln Phe Leu	
100 105 110	
Phe Tyr Arg His Cys Arg Tyr Phe Pro Met Leu Leu Asn His Pro Glu	
115 120 125	
Lys Cys Arg Gly Asp Val Tyr Leu Leu Val Val Val Lys Ser Val Ile	
130 135 140	
Thr Gln His Asp Arg Arg Glu Ala Ile Arg Gln Thr Trp Gly Arg Glu	
145 150 155 160	
Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala Val Arg Thr Leu Phe Leu	
165 170 175	
Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg Thr His Tyr Gln Gln Leu	
180 185 190	
Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp Ile Leu Gln Trp Gly Phe	
195 200 205	
Leu Asp Thr Phe Phe Asn Leu Thr Leu Lys Glu Ile His Phe Leu Lys	
210 215 220	
Trp Leu Asp Ile Tyr Cys Pro His Val Pro Phe Ile Phe Lys Gly Asp	
225 230 235 240	
Asp Asp Val Phe Val Asn Pro Thr Asn Leu Leu Glu Phe Leu Ala Asp	
245 250 255	
Arg Gln Pro Gln Glu Asn Leu Phe Val Gly Asp Val Leu Gln His Ala	
260 265 270	
Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr Tyr Ile Pro Gly Ala Leu	
275 280 285	
Tyr Gly Lys Ala Ser Tyr Pro Tyr Ala Gly Gly Gly Phe Leu	
290 295 300	

Met Ala Gly Ser Leu Ala Arg Arg Leu His His Ala Cys Asp Thr Leu
 305 310 315 320
 Glu Leu Tyr Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu Glu Val
 325 330 335
 Leu Gly Val Gln Pro Thr Ala His Glu Gly Phe Lys Thr Phe Gly Ile
 340 345 350
 Ser Arg Asn Arg Asn Ser Arg Met Asn Lys Glu Pro Cys Phe Phe Arg
 355 360 365
 Ala Met Leu Val Val His Lys Leu Leu Pro Pro Glu Leu Leu Ala Met
 370 375 380
 Trp Gly Leu Val His Ser Asn Leu Thr Cys Ser Arg Lys Leu Gln Val
 385 390 395 400
 Leu

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer for PCR

<400> 10
 cagcagctgc tggcctacga agac

24

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer for PCR

<400> 11
 gcacatgccc agaaagacgt cgtc

24

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer for PCR

<400> 12
 cgttcctggg cctcagtttc ctag

24

<210> 13
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer for PCR

<400> 13
 gaccgacttg acaaccacca gca

23

<210> 14
 <211> 23
 <212> DNA
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 <220>
 <223> Oligonucleotide primer for PCR

 <400> 14
 gtagacatcg cccctgcact tct 23

 <210> 15
 <211> 20
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 <220>
 <223> Oligonucleotide primer for PCR

 <400> 15
 gcccagagct gcgagccgct 20

 <210> 16
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 16
 gcacatgccc agaaagacgt cg 22

 <210> 17
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 17
 ggggacaagt ttgtacaaaa aagcaggctt cgctctcag gggccccagg cct 53

 <210> 18
 <211> 54
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 18
 ggggaccact ttgtacaaga aagctgggtc catgggggct caggagcaag tgcc 54

 <210> 19

<211> 94
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> template for PCR

 <400> 19
 gatcatgcat tttcaagtgc agattttcag cttcctgcta atcagtcct cagtcataat 60
 gtcacgtgga gattacaagg acgacgatga caag 94

 <210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 20
 cgggatccat gcattttcaa gtgcag 26

 <210> 21
 <211> 25
 <212> DNA
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 <220>
 <223> Oligonucleotide primer for PCR

 <400> 21
 ggaattcttg tcatcgctgt ccttg 25

 <210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 22
 ttcttcaagt ggctggacat c 21

 <210> 23
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 23
 gccggtcagc cagaaattc 19

 <210> 24
 <211> 21

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide probe

 <400> 24
 actgccccca cgtccccttc a 21

 <210> 25
 <211> 55
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 25
 ggggacaagt ttgtacaaaa aagcaggctt ctggcgccca gagctgcgag ccgct 55

 <210> 26
 <211> 54
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer for PCR

 <400> 26
 ggggaccact ttgtacaaga aagctggggtc catggggggt caggagcaag tgcc 54

 <210> 27
 <211> 22
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Igk signal sequence

 <400> 27

 Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

 Val Ile Met Ser Arg Gly
 20

 <210> 28
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> FLAG peptide sequence

<400> 28

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5